

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/759,618
Source: IFWO
Date Processed by STIC: 5/4/05

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IFWO

RAW SEQUENCE LISTING

DATE: 05/04/2005

PATENT APPLICATION: US/10/759,618

TIME: 14:17:58

Input Set : N:\Crf3\RULE60\10759618.raw

Output Set : N:\CRF4\05032005\J759618.raw

1 <110> APPLICANT: Rosanne M. Crooke
 2 Mark J. Graham
 3 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL TRIGLYCERIDE TRANSFER
 PROTEIN
 4 EXPRESSION
 5 <130> FILE REFERENCE: ISPH-0591
 6 <140> CURRENT APPLICATION NUMBER: 10/759,618
 7 <141> CURRENT FILING DATE: 2004-01-16
 8 <150> PRIOR APPLICATION NUMBER: US/09/917,963
 9 <151> PRIOR FILING DATE: 2001-07-30
 10 <160> NUMBER OF SEQ ID NOS: 137
 12 <210> SEQ ID NO: 1
 13 <211> LENGTH: 20
 14 <212> TYPE: DNA
 15 <213> ORGANISM: Artificial Sequence
 16 <220> FEATURE:
 17 <223> OTHER INFORMATION: Antisense Oligonucleotide
 18 <400> SEQUENCE: 1
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 22 <211> LENGTH: 20
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Artificial Sequence
 25 <220> FEATURE:
 26 <223> OTHER INFORMATION: Antisense Oligonucleotide
 27 <400> SEQUENCE: 2
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 30 <210> SEQ ID NO: 3
 31 <211> LENGTH: 3392
 32 <212> TYPE: DNA
 33 <213> ORGANISM: Homo sapiens
 34 <220> FEATURE:
 35 <221> NAME/KEY: CDS
 36 <222> LOCATION: (87)...(2771)
 37 <400> SEQUENCE: 3
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 39 gatgcagttg aggattgctg gtcaat atg att ctt ctt gct gtg ctt ttt ctc 113
 40 Met Ile Leu Leu Ala Val Leu Phe Leu
 41 1 5
 42 tgc ttc att tcc tca tat tca gct tct gtt aaa ggt cac aca act ggt 161
 43 Cys Phe Ile Ser Ser Tyr Ser Ala Ser Val Lys Gly His Thr Thr Gly
 44 10 15 20 25
 45 ctc tca tta aat aat gac cgg ctg tac aag ctc acg tac tcc act gaa 209
 46 Leu Ser Leu Asn Asn Asp Arg Leu Tyr Lys Leu Thr Tyr Ser Thr Glu

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47					30					35					40				
48	gtt	ctt	ctt	gat	cgg	ggc	aaa	gga	aaa	ctg	caa	gac	agc	gtg	ggc	tac			257
49	Val	Leu	Leu	Asp	Arg	Gly	Lys	Gly	Lys	Leu	Gln	Asp	Ser	Val	Gly	Tyr			
50					45					50					55				
51	cgc	att	tcc	tcc	aac	gtg	gat	gtg	gcc	tta	cta	tgg	agg	aat	cct	gat			305
52	Arg	Ile	Ser	Ser	Asn	Val	Asp	Val	Ala	Leu	Leu	Trp	Arg	Asn	Pro	Asp			
53					60					65					70				
54	ggt	gat	gat	gac	cag	ttg	atc	caa	ata	acg	atg	aag	gat	gta	aat	gtt			353
55	Gly	Asp	Asp	Asp	Gln	Leu	Ile	Gln	Ile	Thr	Met	Lys	Asp	Val	Asn	Val			
56					75					80					85				
57	gaa	aat	gtg	aat	cag	cag	aga	gga	gag	aag	agc	atc	ttc	aaa	gga	aaa			401
58	Glu	Asn	Val	Asn	Gln	Gln	Arg	Gly	Glu	Lys	Ser	Ile	Phe	Lys	Gly	Lys			
59					90					95			100			105			
60	agc	cca	tct	aaa	ata	atg	gga	aag	gaa	aac	ttg	gaa	gct	ctg	caa	aga			449
61	Ser	Pro	Ser	Lys	Ile	Met	Gly	Lys	Glu	Asn	Leu	Glu	Ala	Leu	Gln	Arg			
62					110					115					120				
63	cct	acg	ctc	ctt	cat	cta	atc	cat	gga	aag	gtc	aaa	gag	ttc	tac	tca			497
64	Pro	Thr	Leu	Leu	His	Leu	Ile	His	Gly	Lys	Val	Lys	Glu	Phe	Tyr	Ser			
65					125					130					135				
66	tat	caa	aat	gag	gca	gtg	gcc	ata	gaa	aat	atc	aag	aga	ggt	ctg	gct			545
67	Tyr	Gln	Asn	Glu	Ala	Val	Ala	Ile	Glu	Asn	Ile	Lys	Arg	Gly	Leu	Ala			
68					140					145					150				
69	agc	cta	ttt	cag	aca	cag	tta	agc	tct	gga	acc	acc	aat	gag	gta	gat			593
70	Ser	Leu	Phe	Gln	Thr	Gln	Leu	Ser	Ser	Gly	Thr	Thr	Asn	Glu	Val	Asp			
71					155					160					165				
72	atc	tct	gga	aat	tgt	aaa	gtg	acc	tac	cag	gct	cat	caa	gac	aaa	gtg			641
73	Ile	Ser	Gly	Asn	Cys	Lys	Val	Thr	Tyr	Gln	Ala	His	Gln	Asp	Lys	Val			
74					170					175					180				
75	atc	aaa	att	aag	gcc	ttg	gat	tca	tgc	aaa	ata	gcg	agg	tct	gga	ttt			689
76	Ile	Lys	Ile	Lys	Ala	Leu	Asp	Ser	Cys	Lys	Ile	Ala	Arg	Ser	Gly	Phe			
77					190					195					200				
78	acg	acc	cca	aat	cag	gtc	ttg	ggt	gtc	agt	tca	aaa	gct	aca	tct	gtc			737
79	Thr	Thr	Pro	Asn	Gln	Val	Leu	Gly	Val	Ser	Ser	Lys	Ala	Thr	Ser	Val			
80					205					210					215				
81	acc	acc	tat	aag	ata	gaa	gac	agc	ttt	gtt	ata	gct	gtg	ctt	gct	gaa			785
82	Thr	Thr	Tyr	Lys	Ile	Glu	Asp	Ser	Phe	Val	Ile	Ala	Val	Leu	Ala	Glu			
83					220					225					230				
84	gaa	aca	cac	aat	ttt	gga	ctg	aat	ttc	cta	caa	acc	att	aag	ggg	aaa			833
85	Glu	Thr	His	Asn	Phe	Gly	Leu	Asn	Phe	Leu	Gln	Thr	Ile	Lys	Gly	Lys			
86					235					240					245				
87	ata	gta	tcg	aag	cag	aaa	tta	gag	ctg	aag	aca	acc	gaa	gca	ggc	cca			881
88	Ile	Val	Ser	Lys	Gln	Lys	Leu	Glu	Leu	Lys	Thr	Thr	Glu	Ala	Gly	Pro			
89					250					255					260				
90	aga	ttg	atg	tct	gga	aag	cag	gct	gca	gcc	ata	atc	aaa	gca	gtt	gat			929
91	Arg	Leu	Met	Ser	Gly	Lys	Gln	Ala	Ala	Ala	Ile	Ile	Lys	Ala	Val	Asp			
92					270					275					280				
93	tca	aag	tac	acg	gcc	att	ccc	att	gtg	ggg	cag	gtc	ttc	cag	agc	cac			977
94	Ser	Lys	Tyr	Thr	Ala	Ile	Pro	Ile	Val	Gly	Gln	Val	Phe	Gln	Ser	His			
95					285					290					295				

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96   tgt aaa gga tgt cct tct ctc tcg gag ctc tgg cgg tcc acc agg aaa   1025
97   Cys Lys Gly Cys Pro Ser Leu Ser Glu Leu Trp Arg Ser Thr Arg Lys
98           300                      305                      310
99   tac ctg cag cct gac aac ctt tcc aag gct gag gct gtc aga aac ttc   1073
100   Tyr Leu Gln Pro Asp Asn Leu Ser Lys Ala Glu Ala Val Arg Asn Phe
101           315                      320                      325
102   ctg gcc ttc att cag cac ctc agg act gcg aag aaa gaa gag atc ctt   1121
103   Leu Ala Phe Ile Gln His Leu Arg Thr Ala Lys Lys Glu Glu Ile Leu
104   330                      335                      340                      345
105   caa ata cta aag atg gaa aat aag gaa gta tta cct cag ctg gtg gat   1169
106   Gln Ile Leu Lys Met Glu Asn Lys Glu Val Leu Pro Gln Leu Val Asp
107           350                      355                      360
108   gct gtc acc tct gct cag acc tca gac tca tta gaa gcc att ttg gac   1217
109   Ala Val Thr Ser Ala Gln Thr Ser Asp Ser Leu Glu Ala Ile Leu Asp
110           365                      370                      375
111   ttt ttg gat ttc aaa agt gac agc agc att atc ctc cag gag agg ttt   1265
112   Phe Leu Asp Phe Lys Ser Asp Ser Ser Ile Ile Leu Gln Glu Arg Phe
113           380                      385                      390
114   ctc tat gcc tgt gga ttt gct tct cat ccc aat gaa gaa ctc ctg aga   1313
115   Leu Tyr Ala Cys Gly Phe Ala Ser His Pro Asn Glu Glu Leu Leu Arg
116           395                      400                      405
117   gcc ctc att agt aag ttc aaa ggt tct att ggt agc agt gac atc aga   1361
118   Ala Leu Ile Ser Lys Phe Lys Gly Ser Ile Gly Ser Ser Asp Ile Arg
119   410                      415                      420                      425
120   gaa act gtt atg atc atc act ggg aca ctt gtc aga aag ttg tgt cag   1409
121   Glu Thr Val Met Ile Ile Thr Gly Thr Leu Val Arg Lys Leu Cys Gln
122           430                      435                      440
123   aat gaa ggc tgc aaa ctc aaa gca gta gtg gaa gct aag aag tta atc   1457
124   Asn Glu Gly Cys Lys Leu Lys Ala Val Val Glu Ala Lys Lys Leu Ile
125           445                      450                      455
126   ctg gga gga ctt gaa aaa gca gag aaa aaa gag gac acc agg atg tat   1505
127   Leu Gly Gly Leu Glu Lys Ala Glu Lys Lys Glu Asp Thr Arg Met Tyr
128           460                      465                      470
129   ctg ctg gct ttg aag aat gcc ctg ctt cca gaa ggc atc cca agt ctt   1553
130   Leu Leu Ala Leu Lys Asn Ala Leu Leu Pro Glu Gly Ile Pro Ser Leu
131           475                      480                      485
132   ctg aag tat gca gaa gca gga gaa ggg ccc atc agc cac ctg gct acc   1601
133   Leu Lys Tyr Ala Glu Ala Gly Glu Gly Pro Ile Ser His Leu Ala Thr
134   490                      495                      500                      505
135   act gct ctc cag aga tat gat ctc cct ttc ata act gat gag gtg aag   1649
136   Thr Ala Leu Gln Arg Tyr Asp Leu Pro Phe Ile Thr Asp Glu Val Lys
137           510                      515                      520
138   aag acc tta aac aga ata tac cac caa aac cgt aaa gtt cat gaa aag   1697
139   Lys Thr Leu Asn Arg Ile Tyr His Gln Asn Arg Lys Val His Glu Lys
140           525                      530                      535
141   act gtg cgc act gct gca gct gct atc att tta aat aac aat cca tcc   1745
142   Thr Val Arg Thr Ala Ala Ala Ala Ile Ile Leu Asn Asn Asn Pro Ser
143           540                      545                      550
144   tac atg gac gtc aag aac atc ctg ctg tct att ggg gag ctt ccc caa   1793

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146		555					560					565					
147	gaa	atg	aat	aaa	tac	atg	ctc	gcc	att	gtt	caa	gac	atc	cta	cgt	ttg	1841
148	Glu	Met	Asn	Lys	Tyr	Met	Leu	Ala	Ile	Val	Gln	Asp	Ile	Leu	Arg	Leu	
149	570					575					580					585	
150	gaa	atg	cct	gca	agc	aaa	att	gtc	cgt	cga	gtt	ctg	aag	gaa	atg	gtc	1889
151	Glu	Met	Pro	Ala	Ser	Lys	Ile	Val	Arg	Arg	Val	Leu	Lys	Glu	Met	Val	
152					590					595					600		
153	gct	cac	aat	tat	gac	cgt	ttc	tcc	agg	agt	gga	tct	tct	tct	gcc	tac	1937
154	Ala	His	Asn	Tyr	Asp	Arg	Phe	Ser	Arg	Ser	Gly	Ser	Ser	Ser	Ala	Tyr	
155				605					610					615			
156	act	ggc	tac	ata	gaa	cgt	agt	ccc	cgt	tcg	gca	tct	act	tac	agc	cta	1985
157	Thr	Gly	Tyr	Ile	Glu	Arg	Ser	Pro	Arg	Ser	Ala	Ser	Thr	Tyr	Ser	Leu	
158			620					625					630				
159	gac	att	ctc	tac	tcg	ggc	tct	ggc	att	cta	agg	aga	agt	aac	ctg	aac	2033
160	Asp	Ile	Leu	Tyr	Ser	Gly	Ser	Gly	Ile	Leu	Arg	Arg	Ser	Asn	Leu	Asn	
161	635					640					645						
162	atc	ttt	cag	tac	att	ggg	aag	gct	ggc	ctt	cac	ggc	agc	cag	gtg	gtt	2081
163	Ile	Phe	Gln	Tyr	Ile	Gly	Lys	Ala	Gly	Leu	His	Gly	Ser	Gln	Val	Val	
164	650					655					660				665		
165	att	gaa	gcc	caa	gga	ctg	gaa	gcc	tta	atc	gca	gcc	acc	cct	gac	gag	2129
166	Ile	Glu	Ala	Gln	Gly	Leu	Glu	Ala	Leu	Ile	Ala	Ala	Thr	Pro	Asp	Glu	
167				670					675						680		
168	ggg	gag	gag	aac	ctt	gac	tcc	tat	gct	ggc	atg	tca	gcc	atc	ctc	ttt	2177
169	Gly	Glu	Glu	Asn	Leu	Asp	Ser	Tyr	Ala	Gly	Met	Ser	Ala	Ile	Leu	Phe	
170				685					690					695			
171	gat	gtt	cag	ctc	aga	cct	gtc	acc	ttt	ttc	aac	gga	tac	agt	gat	ttg	2225
172	Asp	Val	Gln	Leu	Arg	Pro	Val	Thr	Phe	Phe	Asn	Gly	Tyr	Ser	Asp	Leu	
173			700					705					710				
174	atg	tcc	aaa	atg	ctg	tca	gca	tct	ggc	gac	cct	atc	agt	gtg	gtg	aaa	2273
175	Met	Ser	Lys	Met	Leu	Ser	Ala	Ser	Gly	Asp	Pro	Ile	Ser	Val	Val	Lys	
176	715					720					725						
177	gga	ctt	att	ctg	cta	ata	gat	cat	tct	cag	gaa	ctt	cag	tta	caa	tct	2321
178	Gly	Leu	Ile	Leu	Leu	Ile	Asp	His	Ser	Gln	Glu	Leu	Gln	Leu	Gln	Ser	
179	730					735					740				745		
180	gga	cta	aaa	gcc	aat	ata	gag	gtc	cag	ggc	ggc	cta	gct	att	gat	att	2369
181	Gly	Leu	Lys	Ala	Asn	Ile	Glu	Val	Gln	Gly	Gly	Leu	Ala	Ile	Asp	Ile	
182				750					755					760			
183	tca	ggc	gca	atg	gag	ttt	agc	ttg	tgg	tat	cgt	gag	tct	aaa	acc	cga	2417
184	Ser	Gly	Ala	Met	Glu	Phe	Ser	Leu	Trp	Tyr	Arg	Glu	Ser	Lys	Thr	Arg	
185				765					770					775			
186	gtg	aaa	aat	agg	gtg	act	gtg	gta	ata	acc	act	gac	atc	aca	gtg	gac	2465
187	Val	Lys	Asn	Arg	Val	Thr	Val	Val	Ile	Thr	Thr	Asp	Ile	Thr	Val	Asp	
188			780					785					790				
189	tcc	tct	ttt	gtg	aaa	gct	ggc	ctg	gaa	acc	agt	aca	gaa	aca	gaa	gca	2513
190	Ser	Ser	Phe	Val	Lys	Ala	Gly	Leu	Glu	Thr	Ser	Thr	Glu	Thr	Glu	Ala	
191			795				800					805					
192	ggc	ttg	gag	ttt	atc	tcc	aca	gtg	cag	ttt	tct	cag	tac	cca	ttc	tta	2561
193	Gly	Leu	Glu	Phe	Ile	Ser	Thr	Val	Gln	Phe	Ser	Gln	Tyr	Pro	Phe	Leu	

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196      Val Cys Met Gln Met Asp Lys Asp Glu Ala Pro Phe Arg Gln Phe Glu
197      830      835      840
198      aaa aag tac gaa agg ctg tcc aca ggc aga ggt tat gtc tct cag aaa      2657
199      Lys Lys Tyr Glu Arg Leu Ser Thr Gly Arg Gly Tyr Val Ser Gln Lys
200      845      850      855
201      aga aaa gaa agc gta tta gca gga tgt gaa ttc ccg ctc cat caa gag      2705
202      Arg Lys Glu Ser Val Leu Ala Gly Cys Glu Phe Pro Leu His Gln Glu
203      860      865      870
204      aac tca gag atg tgc aaa gtg gtg ttt gcc cct cag ccg gat agt act      2753
205      Asn Ser Glu Met Cys Lys Val Val Phe Ala Pro Gln Pro Asp Ser Thr
206      875      880      885
207      tcc agc gga tgg ttt tga aactgacctg tgatatttta cttgaatttg      2801
208      Ser Ser Gly Trp Phe
209      890
210      tctccccgaa agggacacaa tgtggcatga ctaagtactt gctctctgag agcacagcgt      2861
211      ttacatatattt acctgtattt aagatttttg taaaaagcta caaaaaactg cagtttgatc      2921
212      aaatttgggt atatgcagta tgctaccac agcgtcattt tgaatcatca tgtgacgctt      2981
213      tcaacaacgt tcttagttta cttataacctc tctcaaatct catttggtac agtcagaata      3041
214      gttattctct aagaggaaac tagtgtttgt taaaaacaaa aataaaaaaca aaaccacaca      3101
215      aggagaaccc aattttgttt caacaatttt tgatcaatgt atatgaagct cttgatagga      3161
216      cttccttaag catgacggga aaaccaaaca cgttccctaa tcaggaaaaa aaaaaaaaaa      3221
217      aaaaagtaag acacaaacaa accatttttt tctctttttt tggagttggg ggcccaggga      3281
218      gaagggacaa ggcttttaaa agacttgta gccaaacttca agaattaata tttatgtctc      3341
219      tgttattggt agttttaagc cttaaggtag aaggcacata gaaataacat c      3392
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222 <211> LENGTH: 18
223 <212> TYPE: DNA
224 <213> ORGANISM: Artificial Sequence
225 <220> FEATURE:
226 <223> OTHER INFORMATION: PCR Primer
227 <400> SEQUENCE: 4
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232 <212> TYPE: DNA
233 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <223> OTHER INFORMATION: PCR Primer
236 <400> SEQUENCE: 5
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241 <212> TYPE: DNA
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243 <220> FEATURE:
244 <223> OTHER INFORMATION: PCR Probe
245 <400> SEQUENCE: 6

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 05/04/2005
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The rules require that a line not exceed 72 characters in length. This includes spaces.

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/759,618

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